

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/199,874C

DATE: 11/24/2000
TIME: 14:59:48

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\11242000\I199874C.raw

4 <110> APPLICANT: Segre, Gino V.
5 Kronenberg, Henry M.
6 Abou-Samra, Abdul-Badi
7 Juppner, Harald
8 Potts, Jr., John T.
9 Schipani, Ernestina
11 <120> TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
13 <130> FILE REFERENCE: 00786/071005
15 <140> CURRENT APPLICATION NUMBER: US 09/199,874C
16 <141> CURRENT FILING DATE: 1998-11-24
18 <150> PRIOR APPLICATION NUMBER: US 08/471,494
19 <151> PRIOR FILING DATE: 1995-06-06
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1862
27 <212> TYPE: DNA
28 <213> ORGANISM: Didelphoidea
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (98)...(1642)
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36 gtggccccgt tggactcgcc cctagggAAC ggccggcg 'atg gga gcg ccc cgg atc 115
37 Met Gly Ala Pro Arg Ile
38 1 5
40 tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc 163
41 Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val
42 10 15 20
44 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211
45 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile
46 25 30 35
48 att ctt ctg cgc aat gcc cag gcc cag tgc gag cag cgc ctg aua gag 259
49 Ile Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu
50 40 45 50
52 gtc ctc agg gtc cct gaa ctt gct gaa tct gtc aaa gac tgg atg tca 307
53 Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser
54 55 60 65 70
56 agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc 355
57 Arg Ser Ala Lys Thr Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro
58 75 80 85
60 cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat 403
61 Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp
62 90 95 100
64 ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga 451
65 Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly
66 105 110 115

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H.J.P

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TECH CENTER 1600 2000

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/199,874C

DATE: 11/24/2000
TIME: 14:59:48

Input Set : A:\Sequence.txt
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68	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	tac	gac	499
69	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp		
70	120				125				130									
72	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgq	cgc	tgt	gac	agc	aat	ggc	agc	547	
73	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser		
74	135				140				145				150					
76	tgg	qag	ctg	gtg	cct	ggg	aac	aac	cgq	aca	tgg	gca	aat	tac	agc	gaa	595	
77	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu		
78					155				160				165					
80	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgq	gaa	cgq	aat	tac	agc	gaa	643	
81	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp		
82					170				175				180					
84	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691	
85	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser		
86					185				190				195					
88	ctc	act	gtg	qct	gtg	ctg	att	ctg	ggg	tac	ttt	agg	agg	tta	cat	tgc	739	
89	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys		
90					200				205				210					
92	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgq	787	
93	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Ser	Phe	Met	Leu	Arg			
94	215				220				225				230					
96	gct	gtg	agc	atc	atc	aag	gat	gct	gtg	ctc	tac	tcc	ggg	gtt	tcc		835	
97	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser		
98					235				240				245					
100	aca	gat	gaa	atc	gag	cgc	atc	acc	gag	gag	ctg	agg	ggc	tcc	aca		883	
101	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr		
102					250				255				260					
104	gag	cct	ccc	cct	gct	gac	aag	gct	ggg	ttt	gtg	ggc	tgc	aga	gtg	gct	931	
105	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala		
106					265				270				275					
108	gtt	acc	gtc	ttt	ctt	tac	ttc	ctg	acc	acc	tac	tcc	tgg	atc	ctg		979	
109	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu		
110					280				285				290					
112	gtt	gaa	ggc	ctc	tac	ttt	cac	agc	ctc	atc	ttc	atg	gct	ttt	ttc	tct	1027	
113	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser		
114	295				300				305				310					
116	gag	aaa	aag	tat	ctc	tgg	ggt	ttc	aca	tta	ttt	ggc	tgg	ggc	ctc	cct	1075	
117	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro		
118					315				320				325					
120	gcc	gtg	ttt	gtc	gct	gtg	tgg	gtg	acc	gtg	agg	gct	aca	ctg	ggc	aac	1123	
121	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn		
122					330				335				340					
124	act	gag	tgc	tgg	gac	ctg	agt	tcc	ggg	aat	aag	aaa	tgg	atc	ata	cag	1171	
125	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln		
126					345				350				355					
128	gtt	ccc	atc	ctg	gca	gct	att	gtg	gtg	aac	ttt	att	ctt	ttt	atc	aat	1219	
129	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn		
130					360				365				370					
132	ata	atc	aga	gtc	ctg	gct	act	aaa	ctc	cgq	gag	acc	aat	gca	ggg	aga	1267	

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134	375				380				385						390								
136	tgt	gac	acg	agg	caa	caq	tat	aga	aag	ctg	ctg	aag	tcc	acg	cta	gtc	1315						
137	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val							
138						395				400					405								
140	ctc	atg	ccg	cta	ttt	ggg	gtg	cac	tac	atc	gtc	ttc	atg	gcc	acg	ccg	1363						
141	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro							
142									410		415				420								
144	tac	aca	gaa	gta	tca	ggg	att	ctt	tgg	caa	gtc	caa	atg	cac	tat	gaa	1411						
145	Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gin	Val	Gln	Met	His	Tyr	Glu							
146									425		430				435								
148	atg	ctc	tcc	aat	tca	tcc	cag	ggg	ttt	ttc	gtt	gcc	att	ata	tac	tgt	1459						
149	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys							
150									440		445				450								
152	ttc	tgc	aat	gga	gag	gta	caa	gca	gag	atc	aag	aag	tca	tgg	agc	cga	1507						
153	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg							
154						455			460		465				470								
156	tgg	acc	ctg	gcc	ttg	gac	ttc	aag	cg	aag	gcc	cg	agt	ggc	agc	agt	1555						
157	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser							
158									475		480				485								
160	acc	tac	agc	tat	ggc	ccc	atg	gtg	tca	cat	aca	agt	gtc	acc	aat	gtg	1603						
161	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val							
162									490		495				500								
164	gga	cct	cga	ggg	ggc	tgg	cct	tgt	ccc	tca	gcc	ctc	gac	tagtcttgg		1652							
165	Gly	Pro	Arg	Gly	Gly	Trp	Pro	Cys	Pro	Ser	Ala	Leu	Asp										
166						505			510		515												
168	ggctggagcc	agtgc	ccat	tg	gccc	gttgc	cttgc	ggc	tatgt	ga	atgc	atgg	ttccat			1712							
169	ttctgaga	ac	tcatt	gc	tt	catcty	gccc	agag	cct	ggc	acc	aaa	atgt	acgg	gtat		1772						
170	caatgg	ct	tg	gactt	ttat	g	agc	aat	gtg	ttgg	ttacag	cccc	ctcc	ac	tc	ctggagga	1832						
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184	gtgg	cccc	cg	tgg	act	cc	tc	tgc	tcc	gt	tc	tc	ac	gc	cc	cg	atc	atc	atc	115			
185																	Met	Gly	Ala	Pro	Arg	Ile	
186																	1	5					
188	tgc	cac	agc	ctt	gcc	ttt	ctc	tc	tgc	tgc	tc	tc	ac	tc	tc	gtc							163
189	Ser	His	Ser	Leu	Ala	Leu	Leu	Leu	Cys	Cys	Ser	Val	Leu	Ser	Ser	Val							
190						10			15				20										
192	tac	gca	ctg	gtg	gat	gcc	ttt	gt	tgc	ata	ac	a	ag	g	ag	g	atc						211
193	Tyr	Ala	Leu	Val	Asp	Ala	Asp	Asp	Val	Ile	Thr	Lys	Glu	Glu	Gln	Ile							
194						25			30				35										
196	att	ctt	ctg	cgc	aat	gcc	cag	gcc	cag	tgt	g	at	g	at	cc	ctg	aaa	gag					259

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198	40						45				50						
200	gtc	ctc	agg	gtc	cct	gaa	ctt	qct	gaa	tct	gcc	aaa	gac	tgg	atg	tca	
201	Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
202	55						60				65				70		
204	agg	tct	gca	aag	aca	aag	aag	gag	aaa	cct	gca	gaa	aag	ctt	tat	ccc	
205	Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
206							75				80				85		
208	cag	gca	gag	gag	tcc	agg	gaa	gtt	tct	gac	agg	agc	cgg	ctg	cag	gat	
209	Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
210							90				95				100		
212	ggc	ttc	tgc	cta	cct	gaa	gag	tgg	qac	aac	att	gtg	tgc	tgg	cct	gct	gga
213	Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
214							105				110				115		
216	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	tcc	tac	gac	
217	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
218							120				125				130		
220	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgg	cgc	tgt	qac	agc	aat	ggc	agc	
221	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
222							135				140				145		
224	tgg	gag	ctg	gtg	cct	ggg	aac	aac	egg	aca	tgg	gcg	aat	tac	agc	gaa	
225	Trp	Glu	Ile	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
226							155				160				165		
228	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgg	gaa	cgg	gaa	gtc	ttt	gat	
229	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
230							170				175				180		
232	cgc	ctc	gga	atg	atc	ata	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc
233	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
234							185				190				195		
236	ctc	act	gtg	gtc	ctg	att	ctg	ggt	tac	ttt	agg	agg	tta	cat	tgc		
237	Leu	Thr	Val	Ala	Val	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys		
238							200				205				210		
240	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgg	
241	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
242							215				220				225		
244	gtc	gtt	gtc	atc	atc	aag	gat	gct	gtg	ctc	tac	tcc	ggg	gtt	tcc		
245	Ala	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser
246							235				240				245		
248	aca	gat	gaa	atc	gag	cyc	atc	acc	gag	gag	gag	ctg	agg	gcc	tcc	aca	
249	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
250							250				255				260		
252	gag	cct	ccc	cct	gtc	gac	aag	ggc	ggc	gtt	ttt	gtg	ggc	tgc	aga	gtg	ggc
253	Glu	Pro	Pro	Pro	Ala	Asp	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala		
254							265				270				275		
256	gtc	acc	gtc	tcc	ctt	tac	tcc	ctg	acc	acc	aac	tac	tcc	atc	ctg		
257	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Tyr	Trp	Ile	Leu
258							280				285				290		
260	gtg	gaa	ggc	ctc	tac	ctt	cac	agc	ctc	atc	tcc	atg	gtc	ttt	tcc	tct	
261	Val	Glu	Gly	Ile	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	

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262	295	300	305	310													
264	gag	aaa	aag	tat	ctc	tgg	ggt	ttc	aca	tta	ttt	ggc	tgg	ggc	ctc	cct	1075
265	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Ieu	Pro	
266																	325
268	gcc	gtg	ttt	gtc	gtc	gtg	tgg	gtg	acc	gtg	agg	gtc	aca	ctg	gcc	aac	1123
269	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
270																	340
272	act	gag	tgc	tgg	gac	ctg	agt	tgc	ggg	aat	aag	aaa	tgg	atc	ata	cay	1171
273	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Cln	
274																	355
276	gtg	ccc	atc	ctg	gca	gct	att	gtg	gtg	aac	ttt	att	ctt	ttt	atc	aat	1219
277	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
278																	360
280	ata	atc	aga	gtc	ctg	gct	act	aaa	ctc	cgq	gag	acc	aat	gca	ggg	aga	1267
281	Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
282																	375
284	tgt	gac	acg	agg	caa	caq	tat	aga	aag	ctg	ctg	aag	tcc	acg	cta	gtc	1315
285	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	
286																	395
288	ctc	atg	ccg	cta	ttt	ggg	gtg	cac	tac	atc	gtc	ttc	atq	gcc	acg	ccg	1363
289	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	
290																	410
292	tac	aca	gaa	gta	tca	ggg	att	ctt	tgg	caa	gtc	caa	atg	cac	tat	gaa	1411
293	Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	
294																	425
296	atg	ctc	ttc	aat	tca	ttc	cag	gga	ttt	ttc	gtt	gcc	att	ata	tac	tgt	1459
297	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
298																	440
300	ttc	tgc	aat	gga	gag	gta	caa	gca	gag	atc	aag	tca	tgg	agc	cga		1507
301	Phe	Cys	Asn	Gly	Glu	Val	Glu	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	
302																	455
304	tgg	acc	ctg	gcc	ttg	qac	ttc	aag	cgq	aag	gcc	cgq	agt	ggc	acg	agt	1555
305	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
306																	475
308	acc	tac	agc	tat	ggc	ccc	atg	gtg	tca	cat	aca	agt	gtc	acc	aat	gtg	1603
309	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
310																	490
312	gga	cct	cga	ggg	ggg	ctg	gcc	ttg	tcc	ctc	agc	cct	cga	cta	gtc	cct	1651
313	Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu	Ser	Leu	Ser	Pro	Arg	Leu	Ala	Pro	
314																	505
316	ggg	gct	gga	gcc	agt	gcc	aat	ggc	cat	cac	cag	ttg	cct	ggc	tat	gtg	1699
317	Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly	His	His	Gln	Leu	Pro	Gly	Tyr	Val	
318																	520
320	aag	cat	ggt	tcc	att	tct	gag	aac	tca	ttg	cct	tca	tct	ggc	cca	gag	1747
321	Lys	His	Gly	Ser	Ile	Ser	Glu	Asn	Ser	Leu	Pro	Ser	Ser	Gly	Pro	Glu	
322																	535
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325	Pro	Gly	Thr	Lys	Asp	Asp	Gly	Tyr	Leu	Asn	Gly	Ser	Gly	Leu	Tyr	Glu	
326																	555

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Input Set : A:\Sequence.txt
Output Set: N:\CRF3\11242000\I199874C.raw

L:724 M:341 W: (46) "0" or "Xaa" used, for SEQ TD#:8